

SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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 HIBI, Masahiko
 LIN, Anning

<120> ONCOPROTEIN PROTEIN KINASE

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<140> US 10/051,989

<141> 2002-01-16

<150> US 09/461,649

<151> 1999-12-14

<150> US 09/150,201

<151> 1998-09-08

<150> US 08/799,913

<151> 1997-02-13

<150> US 08/444,393

<151> 1995-05-19

<150> US 08/276,860

<151> 1994-07-18

<150> US 08/220,602

<151> 1994-03-25

<150> US 08/094,533

<151> 1993-07-19

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 47

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 1

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Leu	Lys	Pro	His	Leu	Arg	Ala	Lys	Asn	Ser	Asp	Leu	Leu	Thr	Ser	Pro
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Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu
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33

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 gcgcacgaag agccgtcagt gagtgaccgc gacttttcaa agccgggtag ggcgcgcgag 180
 tcgacaagta agagtgcggg aggcattctta attaaccttg cgctccctgg agcagctggt 240
 gaggagggcg cacgggggacg acagccagcg ggtgcgtgcg ctcttagaga aactttccct 300
 gtcaaaggct ccggggggcg cgggtgtccc ccgcttgcca cagccctggt gcggccccga 360
 aacttgtgcg cgcacgccaa actaacctca cgtgaagtga cggactgttc t atg act 417
 Met Thr
 1
 gca aag atg gaa acg acc ttc tat gac gat gcc ctc aac gcc tcg ttc 465
 Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser Phe
 5 10 15
 ctc ccg tcc gag agc gga cct tat ggc tac agt aac ccc aag atc ctg 513
 Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile Leu
 20 25 30
 aaa cag agc atg acc ctg aac ctg gcc gac cca gtg ggg agc ctg aag 561
 Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu Lys
 35 40 45 50

ccg cac ctc cgc gcc aag aac tcg gac ctc ctc acc tcg ccc gac gtg Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val	609
55 60 65	
ggg ctg ctc aag ctg gcg tcg ccc gag ctg gag cgc ctg ata atc cag Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln	657
70 75 80	
tcc agc aac ggg cac atc acc acc acg ccg acc ccc acc cag ttc ctg Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe Leu	705
85 90 95	
tgc ccc aag aac gtg aca gat gag cag gag ggg ttc gcc gag ggc ttc Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe	753
100 105 110	
gtg cgc gcc ctg gcc gaa ctg cac agc cag aac acg ctg ccc agc gtc Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser Val	801
115 120 125 130	
acg tcg gcg gcg cag ccg gtc aac ggg gca ggc atg gtg gct ccc gcg Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala	849
135 140 145	
gta gcc tcg gtg gca ggg ggc agc ggc agc ggc ggc ttc agc gcc agc Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser	897
150 155 160	
ctg cac agc gag ccg ccg gtc tac gca aac ctc agc aac ttc aac cca Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn Pro	945
165 170 175	
ggc gcg ctg agc agc ggc ggc ggg gcg ccc tcc tac ggc gcg gcc ggc Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala Gly	993
180 185 190	
ctg gcc ttt ccc gcg caa ccc cag cag cag cag cag cag ccg ccg cac cac Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro His His	1041
195 200 205 210	
ctg ccc cag cag atg ccc gtg cag cac ccg cgg ctg cag gcc ctg aag Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu Lys	1089
215 220 225	
gag gag cct cag aca gtg ccc gag atg ccc ggc gag aca ccg ccc ctg Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro Pro Leu	1137
230 235 240	
tcc ccc atc gac atg gag tcc cag gag cgg atc aag gcg gag agg aag Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg Lys	1185
245 250 255	
cgc atg agg aac cgc atc gct gcc tcc aag tgc cga aaa agg aag ctg Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys Leu	1233
260 265 270	
gag aga atc gcc cgg ctg gag gaa aaa gtg aaa acc ttg aaa gct cag Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln	1281
275 280 285 290	
aac tcg gag ctg gcg tcc acg gcc aac atg ctc agg gaa cag gtg gca	1329

Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala
 295 300 305

cag ctt aaa cag aaa gtc atg aac cac gtt aac agt ggg tgc caa ctc 1377
 Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys Gln Leu
 310 315 320

atg cta acg cag cag ttg caa aca ttt tgaagagaga ccgtcggggg 1424
 Met Leu Thr Gln Gln Leu Gln Thr Phe
 325 330

ctgagggggca acgaagaaaa aaaataacac agagagacag acttgagaac ttgacaagtt 1484

gcgacggaga gaaaaaagaa gtgtccgaga actaaagcca agggatatcca agttggactg 1544

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cggcaggagg gaggtttgtg agagcgaggc tgagcctaca gatgaactct ttctggcctg 1904

ctttcgttaa ctgtgtatgt acatatatat attttttaat ttgattaaag ctgattactg 1964

tcaataaaca gcttcatgcc tttgtaagtt atttcttggt tgtttgtttg ggatcctgcc 2024

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tataattttt tt 2096

<210> 10
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Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
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Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
 35 40 45

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
 50 55 60

Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
 65 70 75 80

Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
85 90 95

Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
100 105 110

Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
115 120 125

Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
130 135 140

Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
145 150 155 160

Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
165 170 175

Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
180 185 190

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
195 200 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
210 215 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225 230 235 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
245 250 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
260 265 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
275 280 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
290 295 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe
325 330